

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/135,988

DATE: 08/24/98
TIME: 15:51:52

INPUT SET: S28228.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

- 1
- 2
- 3 (1) General Information
- 4
- 5 (i) APPLICANT: Bryan, Bruce
- 6
- 7 (ii) TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
- 8
- 9 (iii) NUMBER OF SEQUENCES: 14
- 10
- 11 (iv) CORRESPONDENCE ADDRESS:
- 12 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
- 13 (B) STREET: 4250 Executive Square, 7th Floor
- 14 (C) CITY: La Jolla
- 15 (D) STATE: CA
- 16 (E) COUNTRY: USA
- 17 (F) ZIP: 92037
- 18
- 19 (v) COMPUTER READABLE FORM:
- 20 (A) MEDIUM TYPE: Diskette
- 21 (B) COMPUTER: IBM Compatible
- 22 (C) OPERATING SYSTEM: DOS
- 23 (D) SOFTWARE: FastSEQ Version 1.5
- 24
- 25 (vi) CURRENT APPLICATION DATA:
- 26 (A) APPLICATION NUMBER:
- 27 (B) FILING DATE:
- 28 (C) CLASSIFICATION:
- 29
- 30 (vii) PRIOR APPLICATION DATA:
- 31 (A) APPLICATION NUMBER: 08/757,046
- 32 (B) FILING DATE: 11-25-96
- 33 (C) CLASSIFICATION:
- 34
- 35 (vii) PRIOR APPLICATION DATA:
- 36 (A) APPLICATION NUMBER: 08/597,274
- 37 (B) FILING DATE: 02-06-96
- 38
- 39 (viii) ATTORNEY/AGENT INFORMATION:
- 40 (A) NAME: Seidman, Stephanie L
- 41 (B) REGISTRATION NUMBER: 33,779
- 42 (C) REFERENCE/DOCKET NUMBER: 24727-105C
- 43
- 44 (ix) TELECOMMUNICATION INFORMATION:
- 45 (A) TELEPHONE: 619-450-8400
- 46 (B) TELEFAX: 619-450-8499

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47 (C) TELEX:

48

49 (2) INFORMATION FOR SEQ ID NO:1:

50

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1196 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

56

57 (ii) MOLECULE TYPE: cDNA

58

59 (vi) ORIGINAL SOURCE:

60

61 (ix) FEATURE:

62

63 (A) NAME/KEY: Coding Sequence

64 (B) LOCATION: 1...942

65 (D) OTHER INFORMATION: Renilla Reinformis Luciferase

66

67 (x) PUBLICATION INFORMATION:

68

69 PATENT NO.: 5,418,155

70

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

72

73 AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG 48

74 Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg

75 1 5 10 15

76

77 ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT 96

78 Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val

79 20 25 30

80

81 CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT 144

82 Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn

83 35 40 45

84

85 GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA 192

86 Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg

87 50 55 60

88

89 CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT 240

90 His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp

91 65 70 75 80

92

93 CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG 288

94 Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg

95 85 90 95

96

97 TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT 336

98 Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile

99 100 105 110

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100																	
101	TAC	CAA	AGA	AGA	TCA	TTT	TTT	GTC	GGC	CAT	GAT	TGG	GGT	GCT	TGT	TTG	384
102	Tyr	Gln	Arg	Arg	Ser	Phe	Phe	Val	Gly	His	Asp	Trp	Gly	Ala	Cys	Leu	
103			115					120					125				
104																	
105	GCA	TTT	CAT	TAT	AGC	TAT	GAG	CAT	CAA	GAT	AAG	ATC	AAA	GCA	ATA	GTT	432
106	Ala	Phe	His	Tyr	Ser	Tyr	Glu	His	Gln	Asp	Lys	Ile	Lys	Ala	Ile	Val	
107		130					135					140					
108																	
109	CAC	GCT	GAA	AGT	GTA	GTA	GAT	GTG	ATT	GAA	TCA	TGG	GAT	GAA	TGG	CCT	480
110	His	Ala	Glu	Ser	Val	Val	Asp	Val	Ile	Glu	Ser	Trp	Asp	Glu	Trp	Pro	
111	145					150					155					160	
112																	
113	GAT	ATT	GAA	GAA	GAT	ATT	GCG	TTG	ATC	AAA	TCT	GAA	GAA	GGA	GAA	AAA	528
114	Asp	Ile	Glu	Glu	Asp	Ile	Ala	Leu	Ile	Lys	Ser	Glu	Glu	Gly	Glu	Lys	
115					165					170					175		
116																	
117	ATG	GTT	TTG	GAG	AAT	AAC	TTC	TTC	GTG	GAA	ACC	ATG	TTG	CCA	TCA	AAA	576
118	Met	Val	Leu	Glu	Asn	Asn	Phe	Phe	Val	Glu	Thr	Met	Leu	Pro	Ser	Lys	
119				180					185					190			
120																	
121	ATC	ATG	AGA	AAG	TTA	GAA	CCA	GAA	GAA	TTT	GCA	GCA	TAT	CTT	GAA	CCA	624
122	Ile	Met	Arg	Lys	Leu	Glu	Pro	Glu	Glu	Phe	Ala	Ala	Tyr	Leu	Glu	Pro	
123			195					200					205				
124																	
125	TTC	AAA	GAG	AAA	GGT	GAA	GTT	CGT	CGT	CCA	ACA	TTA	TCA	TGG	CCT	CGT	672
126	Phe	Lys	Glu	Lys	Gly	Glu	Val	Arg	Arg	Pro	Thr	Leu	Ser	Trp	Pro	Arg	
127		210					215					220					
128																	
129	GAA	ATC	CCG	TTA	GTA	AAA	GGT	GGT	AAA	CCT	GAC	GTT	GTA	CAA	ATT	GTT	720
130	Glu	Ile	Pro	Leu	Val	Lys	Gly	Gly	Lys	Pro	Asp	Val	Val	Gln	Ile	Val	
131	225					230					235					240	
132																	
133	AGG	AAT	TAT	AAT	GCT	TAT	CTA	CGT	GCA	AGT	GAT	GAT	TTA	CCA	AAA	ATG	768
134	Arg	Asn	Tyr	Asn	Ala	Tyr	Leu	Arg	Ala	Ser	Asp	Asp	Leu	Pro	Lys	Met	
135					245					250					255		
136																	
137	TTT	ATT	GAA	TCG	GAT	CCA	GGA	TTC	TTT	TCC	AAT	GCT	ATT	GTT	GAA	GGC	816
138	Phe	Ile	Glu	Ser	Asp	Pro	Gly	Phe	Phe	Ser	Asn	Ala	Ile	Val	Glu	Gly	
139				260					265								

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153 CATTTCCTCC GGGTTTAATA ATATAAATGT CATTTCCTCAAC AATTTTATTT TAACTGAATA 1025
154 TTTCACAGGG AACATTCATA TATGTTGATT AATTTAGCTC GAACTTTACT CTGTCATATC 1085
155 ATTTTGGAAT ATTACCTCTT TCAATGAAAC TTTATAAACA GTGGTTCAAT TAATTAATAT 1145
156 ATATTATAAT TACATTTGTT ATGTAATAAA CTCGGTTTTA TTATAAAAAA A 1196

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1665
- (D) OTHER INFORMATION: Cypridina hilgendorffii luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

180 ATG AAG CTA ATA ATT CTG TCT ATT ATA TTG GCC TAC TGT GTC ACA GTC 48
181 Met Lys Leu Ile Ile Leu Ser Ile Ile Leu Ala Tyr Cys Val Thr Val
182 1 5 10 15
183
184 AAC TGC CAG GAT GCA TGT CCT GTA GAA GCT GAA GCA CCG TCA AGT ACA 96
185 Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr
186 20 25 30
187
188 CCA ACA GTC CCA ACA TCT TGT GAA GCT AAA GAA GGA GAA TGT ATC GAT 144
189 Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
190 35 40 45
191
192 ACC AGA TGC GCA ACA TGT AAA CGA GAC ATA CTA TCA GAC GGA CTG TGT 192
193 Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
194 50 55 60
195
196 GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTA ATT 240
197 Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
198 65 70 75 80
199
200 GAA TCC AGA GTA GAA GCT GCT GGA TAT TTT AGA ACG TTT TAC GCC AAA 288
201 Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys
202 85 90 95
203
204 AGA TTT AAT TTT CAG GAA CCT GGT AAA TAT GTG CTG GCT CGA GGA ACC 336
205 Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr

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	100	105	110	
206				
207				
208	AAG GGT GGC GAC TGG TCT GTA ACC CTC ACC ATG GAG AAT CTA GAT GGA			384
209	Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly			
210	115	120	125	
211				
212	CAG AAG GGA GCT GTA CTG ACT AAG ACA ACA CTG GAG GTA GTA GGA GAC			432
213	Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Val Gly Asp			
214	130	135	140	
215				
216	GTA ATA GAC ATT ACT CAA GCT ACT GCA GAT CCT ATC ACA GTT AAC GGA			480
217	Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly			
218	145	150	155	160
219				
220	GGA GCT GAC CCA GTT ATC GCT AAC CCG TTC ACA ATT GGT GAG GTG ACC			528
221	Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr			
222	165	170	175	
223				
224	ATT GCT GTT GTC GAA ATA CCC GGC TTC AAT ATT ACA GTC ATC GAA TTC			576
225	Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe			
226	180	185	190	
227				
228	TTT AAA CTA ATC GTG ATA GAT ATT CTG GGA GGA AGA TCT GTG AGA ATT			624
229	Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile			
230	195	200	205	
231				
232	GCT CCA GAC ACA GCA AAC AAA GGA CTG ATA TCT GGT ATC TGT GGT AAT			672
233	Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn			
234	210	215	220	
235				
236	CTG GAG ATG AAT GAC GCT GAT GAC TTT ACT ACA GAC GCA GAT CAG CTG			720
237	Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu			
238	225	230	235	240
239				
240	GCG ATC CAA CCC AAC ATA AAC AAA GAG TTC GAC GGC TGC CCA TTC TAC			768
241	Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr			
242	245	250	255	
243				
244	GGG AAT CCT TCT GAT ATC GAA TAC TGC AAA GGT CTC ATG GAG CCA TAC			816
245	Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr			
246	260	265	270	
247				
248	AGA GCT GTA TGT CGT AAC AAT ATC AAC TTC TAC TAT TAC ACT CTG TCC			864
249	Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Thr Leu Ser			
250	275	280	285	
251				
252	TGC GCC TTC GCT TAC TGT ATG GGA GGA GAA GAA AGA GCT AAA CAC GTC			912
253	Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val			
254	290	295	300	
255				
256	CTT TTC GAC TAT GTT GAG ACA TGC GCT GCA CCG GAA ACG AGA GGA ACG			960
257	Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr			
258	305	310	315	320

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/135,988

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Line

Error

Original Text